The guanosine monophosphate synthetase (GMPS; EC 6.3.5.2) cDNA coding region was obtained by PCR amplification of cDNA from the SL.1NFLS human fetal spleen/liver cDNA library (Research Genetics). The primers for GMPS cDNA were **SEQ ID No. 1:** 5'-ACATCCCATGGCTCTGTGCAACGG-3' and **SEQ ID No. 2:** 5'-GCATCCCGGGTTACTCCCACTCAGTAG-3'. The 2082 bp GMPS cDNA PCR product was subcloned into pBluescript SK+ (Stratagene). 5μg of this insert were excised and treated with DNase I (Worthington) in 50mM Tris-HCl pH 8, 10mM $MnCl_2$, and 0.005 units DNase I in a 50μl reaction, until fragments were estimated to be at an average length of 300 bps. The reaction was stopped by adding an equal volume of phenol/chloroform, extraction, and ethanol precipitation. The DNA fragments were then blunted using T4 DNA polymerase (New England Biolabs).

The adaptor encoding initiating ATG in all three reading frames, and a *HindIII* recognition sequence, was prepared by annealing the oligonucleotides **SEQ ID No. 3:** P1-5' AAACAAGCTTACCATGGATGGATGG-3' and **SEQ ID No. 4:** P2-5'-CCATCCATCCATGGTAAGCTTG-3'. The adaptor with a translation termination codon in all three reading frames and a *XhoI* recognition sequence, was prepared by annealing oligonucleotides **SEQ ID No. 5:** P3-5'-TAGTTAGTTAGCTCGAGTGC-3' and **SEQ ID No. 6:** P4-5'-AAAGCACTCGAGCTAACTAACTA-3'. Ligation of the cDNA fragments to the adaptors was carried out overnight at 16°C with T4 DNA ligase (New England Biolabs). The ligated fragments were then PCR amplified using primers P1 and P4. PCR products were digested with *XhoI* and *HindIII*, electrophoresed, and products that were larger than 100 bps in length were excised/extracted from agarose gels, and then subcloned into pREP9 (Invitrogen), the former site being proximal to the RSV promoter. Library DNA was prepared from several thousands bacterial colonies.--

REMARKS

In the May 23, 2003 Communication the Examiner asserted that Applicants failed to comply with the requirements of 37 C.F.R. 1.821 through 1.825.

In response, Applicants submit herewith a copy of the Notice to Comply; and the Sequence Listing on a paper and computer readable format in compliance with the requirements of §1.821 through 1.825. The computer readable form containing the nucleic acid and/or amino acid sequences as required by 37 C.F.R. §1.821(f) contains the same information, which is submitted as Sequence Listing, the Sequence Listing complies with the requirements of 37 C.F.R. §1.824 and does not contain any new matter. Thus, Applicants Specification is in compliance with 37 C.F.R. §1.821 through 1.825. Therefore, Applicants respectfully request the Examiner to reconsider and withdraw the objection.

If any additional fee is required, the undersigned Attorney hereby authorizes the United States Patent and Trademark Office to charge such fee to Deposit Account No. 05-0649.

If the Examiner has any comment as to the form content or entry of this paper, the Examiner is requested to contact the undersigned.

Respectfully submitted,

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